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Conference Abstract

Synospecies, an application to reflect changes in taxonomic names based on a triple store based on taxonomic data liberated from publication

Reto Gmür‡, Donat Agosti§

‡ Factsmission, Biel, Switzerland
§ Plazi, Bern, Switzerland

Corresponding author: Reto Gmür (reto@factsmission.com)

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Abstract

Taxonomic treatments, sections of publications documenting the features or distribution of a related group of organisms (called a “taxon”, plural “taxa”) in ways adhering to highly formalized conventions, and published in scientific journals, shape our understanding of global biodiversity (Catapano 2019).

Treatments are the building blocks of the evolving scientific consensus on taxonomic entities. The semantics of these treatments and their relationships are highly structured: taxa are introduced, merged, made obsolete, split, renamed, associated with specimens and so on. Plazi makes this content available in machine-readable form using Resource Description Framework (RDF). RDF is the standard model for Linked Data and the Semantic Web. RDF can be exchanged in different formats (aka concrete syntaxes) such as RDF/XML or Turtle. The data model describes graph structures and relies on Internationalized Resource Identifiers (IRIs), ontologies such as Darwin Core basic vocabulary are used to assign meaning to the identifiers. For Synospecies, we unite all treatments into one large knowledge graph, modelling taxonomic knowledge and its evolution with complete references to quotable treatments. However, this knowledge graph expresses much more than any individual treatment could convey because every referenced entity is linked to every other relevant treatment. On synospecies.plazi.org, we provide a user-friendly

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interface to find the names and treatments related to a taxon. An advanced mode allows execution of queries using the SPARQL query language.

Keywords

biodiversity, RDF, knowledge graph, treatment citation, ontology, Linked Data, SPARQL

Presenting author

Reto Gmür

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